AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting on page 18, line 5, of the application as originally filed with the following, amended paragraph:

Among the 491 granulocyte-selective transcripts listed in Figures 6A-6R, 4 ion channels, 19 GPR and 28 other receptors were further selected (Figure 3). When plural transcripts obtained by different probe sets had identical Genebank or Unigene accession numbers (~~http://~~www.ncbi.nlm.nih.gov/), the transcript showing the highest expression level was selected.

Please replace the paragraph starting on page 18, line 18, of the application as originally filed with the following, amended paragraph:

Among the 51 granulocyte-selective transcripts for ion channels and receptors, we identified 17 granulocyte-selective transcripts that have not been reported for their selective expression (shown in bold letters in Figure 3). Of these 17 transcripts, eight were preferentially expressed by granulocytes other than neutrophils. Among these eight transcripts, the two transcripts for fibroblast growth factor receptor 2 and low density lipoprotein receptor were found to be expressed by multiple tissue cell types (shown at the Web site ~~http://~~www.lsbm.org/index_e.html), which displays genomic expression of 55 different human tissue cells such as brain, heart and lung cells using the same experimental system. Affymetrix, U133A as ourts. Thus, they may not be suitable as a drug target because important organs that are unrelated to allergic inflammation (such as the brain) express it. Among the six novel transcripts found to be preferentially expressed by granulocytes except for neutrophils, we focus on the following four transcripts expressed by granulocytes including basophils. They were Ca^{2+} channel (*CACNA1D*), a prostaglandin E receptor, (*EP3A2)*, epidermal growth factor-like module-containing mucin-like receptor (EMR) 1 (*EMR1*), and HTm4 (*MS4A3*).

Please replace the paragraph starting on page 21, line 4, of the application as originally filed with the following, amended paragraph:

We unexpectedly found 17 granulocyte-selective transcripts including HTm4. Basophil- and/or eosinophil-selective transcripts identified in our study could be potential therapeutic targets for allergic diseases because these granulocytes play a crucial role in allergic inflammation. [1,2] Granulocyte-selective transcripts could also be drug targets for other inflammatory diseases such as systemic vasculitis. [3,4] Analysis of cell type-selective transcripts from database searches is expected to minimize the efforts required for drug discovery. The public database (~~http://~~www.lsbm.org/index_e.html) shows that some granulocyte-selective transcripts (18 out of 51) detected in our study are abundantly expressed by multiple (more than 3) organ tissue cell types using the same GeneChip U133A probe array. Thus, the safety of any candidate drug must be evaluated by comparing its efficacy (on granulocytes) with its toxicity (to organs). Six out of the 17 novel granulocyte-selective molecules may be excluded from drug development due to their expression in multiple organs unrelated to the diseases. Thus, our approach has identified 11 receptors and ion channels with therapeutic potential. Especially, among the 11 receptors and ion channels, seven were basophil- and/or eosinophil-selective and were not expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

Please replace footnote a. of Table 1 on page 27, line 11, of the application as originally filed with the following, amended footnote:

a. The GenBank accession number (~~http://~~www.ncbi.nlm.nih.gov).